

SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> Maize Orthologues of Bacterial RuvB:
cDNAs and Uses Thereof

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<151> 1999-07-16

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Ser Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly
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ctc gac gcc aat ggg atg gcg att gcg ttg gcg gcg ggg ttc gtg ggc      207
Leu Asp Ala Asn Gly Met Ala Ile Ala Leu Ala Ala Gly Phe Val Gly
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cag tcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg att cgc      255
Gln Ser Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg
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cag aaa aag atg gcc ggc cgc gcg gtg ctc ctt gtg ggt ccg ccc gcc      303
Gln Lys Lys Met Ala Gly Arg Ala Val Leu Leu Val Gly Pro Pro Ala
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acg ggc aag acg gcg cta gcg ctc ggc ata gcc cag gag ctc ggc agc      351
Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser
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aag gtc cct ttc tgc cct atg gta gga tca gaa gtg tac tcc tcg gag      399
Lys Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Ser Glu
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gtc aag aaa act gag gtg ctg atg gaa aat ttc cgt aga gct ata ggt      447
Val Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala Ile Gly
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ctt Leu	tcc Ser	cca Pro 140	gaa Glu	gag Glu	gct Ala	gag Glu	agt Ser 145	aca Thr	act Thr	gg Gly	gga Gly	tat Tyr 150	gca Ala	aaa Lys	agc Ser	543
att Ile	agc Ser 155	cat His	gta Val	atc Ile	atc Ile	agc Ser 160	tta Leu	aag Lys	act Thr	gtt Val	aaa Lys 165	ggg Gly	act Thr	aag Lys	caa Gln	591
ctg Leu 170	aag Lys	tta Leu	gat Asp	tct Ser	tca Ser 175	att Ile	tat Tyr	gat Asp	gct Ala	ctg Leu 180	atc Ile	aag Lys	gaa Glu	aag Lys	gtg Val 185	639
gca Ala	gtg Val	gg Gly	gat Asp	gtt Val 190	ata Ile	tac Tyr	att Ile	gaa Glu	gca Ala 195	aat Asn	agt Ser	gga Gly	gca Ala	gtg Val 200	aaa Lys	687
aga Arg	gtt Val	gg Gly	aga Arg 205	tgt Cys	gat Asp	tct Ser	ttt Phe 210	gct Ala	aca Thr	gaa Glu	tac Tyr	gat Asp 215	ctt Leu	gaa Glu	gct Ala	735
gaa Glu	gaa Glu	tat Tyr 220	gtt Val	cct Pro	atc Ile	ccc Pro	aaa Lys 225	gg Gly	gaa Glu	gtc Val	cat His	aag Lys 230	aaa Lys	aaa Lys	gaa Glu	783
ata Ile 235	gtg Val	cag Gln	gat Asp	gtc Val	aca Thr	ctt Leu 240	cat His	gac Asp	ctt Leu	gat Asp	gca Ala 245	gca Ala	aat Asn	gct Ala	cag Gln	831
cca Pro 250	caa Gln	gg Gly	ggc Gly	caa Gln	gat Asp 255	att Ile	ttg Leu	tcc Ser	ctt Leu	atg Met 260	ggc Gly	cag Gln	atg Met	atg Met	aaa Lys 265	879
cca Pro	cga Arg	aag Lys	act Thr 270	gaa Glu	atc Ile	acc Thr	gaa Glu	aaa Lys	cta Leu 275	cgc Arg	caa Gln	gaa Glu	att Ile	aat Asn 280	aag Lys	927
gtg Val	gta Val	aat Asn 285	aga Arg	tat Tyr	atc Ile	gat Asp	gaa Glu	gga Gly 290	att Ile	gca Ala	gag Glu	ctt Leu	gta Val 295	cct Pro	gg Gly	975
gtt Val	tta Leu	ttc Phe 300	att Ile	gac Asp	gag Glu	gtc Val	cac His 305	atg Met	ttg Leu	gat Asp	atc Ile	gaa Glu 310	tgt Cys	ttt Phe	tct Ser	1023
tat Tyr	ctt Leu 315	aac Asn	cg Arg	gca Ala	ttg Leu	gag Glu 320	agc Ser	cca Pro	tta Leu	tca Ser	cca Pro 325	att Ile	gtg Val	ata Ile	ctt Leu	1071
gct Ala 330	acg Thr	aat Asn	agg Arg	gga Gly	ata Ile 335	tgt Cys	aat Asn	gta Val	aga Arg	gga Gly 340	act Thr	gat Asp	atg Met	aca Thr	agt Ser 345	1119
cca Pro	cat His	gg Gly	ata Ile 350	cca Pro	gtg Val	gat Asp	ctt Leu	cta Leu 355	gat Asp	agg Arg	ttg Leu	gtg Val	att Ile	att Ile 360	cgg Arg	1167

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gca caa gtg gag gac att gat atg gat gaa gaa agt ctt gct tat tta 1263
 Ala Gln Val Glu Asp Ile Asp Met Asp Glu Glu Ser Leu Ala Tyr Leu
 380 385 390

ggc gag atc gga cag cag aca tct tta aga cat gct att caa ttg ata 1311
 Gly Glu Ile Gly Gln Gln Thr Ser Leu Arg His Ala Ile Gln Leu Ile
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 Lys Ala Asp Leu Glu Glu Val Ser Gly Leu Tyr Leu Asp Ala Lys Ser
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tcg gct cgg ctg ctc cag gag caa caa gaa aga tac atc acc 1449
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 445 450 455

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 35 40 45
 Ala Gly Leu Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg
 50 55 60
 Ala Val Leu Leu Val Gly Pro Pro Ala Thr Gly Lys Thr Ala Leu Ala
 65 70 75 80
 Leu Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met
 85 90 95
 Val Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu
 100 105 110
 Met Glu Asn Phe Arg Arg Ala Ile Gly Leu Arg Ile Lys Glu Asn Lys
 115 120 125
 Glu Val Tyr Glu Gly Glu Val Thr Glu Leu Ser Pro Glu Glu Ala Glu
 130 135 140
 Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile Ser
 145 150 155 160
 Leu Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Ser Ser Ile
 165 170 175
 Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr
 180 185 190

002090" 060700

Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser
 195 200 205
 Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro
 210 215 220
 Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu
 225 230 235 240
 His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile
 245 250 255
 Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr
 260 265 270
 Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp
 275 280 285
 Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val
 290 295 300
 His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu
 305 310 315 320
 Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys
 325 330 335
 Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val Asp
 340 345 350
 Leu Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro Thr
 355 360 365
 Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Asp Ile Asp
 370 375 380
 Met Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr
 385 390 395 400
 Ser Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser
 405 410 415
 Lys Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val
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 <222> (94)...(1458)

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 1 5

 tcg acc tcg aag aag cag cgc atc gcc acc cac acc cac atc aag gga 162
 Ser Thr Ser Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly
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 ctc ggc ctc gac gcc aat ggg atg gcg att gcg ttg gcg gcg ggg ttc 210
 Leu Gly Leu Asp Ala Asn Gly Met Ala Ile Ala Leu Ala Ala Gly Phe
 25 30 35

 gtg ggc cag gcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg 258
 Val Gly Gln Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met
 40 45 50 55

09589510.060700

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ccc gcc acg ggc aag acg gcg cta gcg ctc ggc ata gcc cag gag ctc Pro Ala Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu 75 80 85	354
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act gaa ctt tcc cca gaa gag gct gag agt aca act ggt gga tat gca Thr Glu Leu Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala 140 145 150	546
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ttt tct tat ctt aac cgt gca ttg gag agc cca tta tca cca atc gtg 1074
 Phe Ser Tyr Leu Asn Arg Ala Leu Glu Ser Pro Leu Ser Pro Ile Val
 315 320 325

ata ctt gct aca aat agg gga ata tgt aat gta aga gga act gat atg 1122
 Ile Leu Ala Thr Asn Arg Gly Ile Cys Asn Val Arg Gly Thr Asp Met
 330 335 340

aca agt cca cat ggt ata ccg gtg gat ctt cta gat agg ctg gtg att 1170
 Thr Ser Pro His Gly Ile Pro Val Asp Leu Leu Asp Arg Leu Val Ile
 345 350 355

att cgg aca gag aca tat ggc cct act gag atg ata cag ata ttg gct 1218
 Ile Arg Thr Glu Thr Tyr Gly Pro Thr Glu Met Ile Gln Ile Leu Ala
 360 365 370 375

atc cga gca caa gtg gag gag att gat atg gat gaa gaa agt ctt gct 1266
 Ile Arg Ala Gln Val Glu Glu Ile Asp Met Asp Glu Glu Ser Leu Ala
 380 385 390

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 Tyr Leu Gly Glu Ile Gly Gln Gln Thr Ser Leu Arg His Ala Ile Gln
 395 400 405

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 Leu Ile Ser Pro Ala Ser Val Val Ser Lys Thr Asn Gly Arg Glu Lys
 410 415 420

atc tgc aag gct gat ctc gag gaa gtc agt ggg ctc tat ttg gat gcc 1410
 Ile Cys Lys Ala Asp Leu Glu Glu Val Ser Gly Leu Tyr Leu Asp Ala
 425 430 435

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 Ala Gly Leu Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg

004090"0F5855

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Leu Gly Ile Ala Gln Glu	Leu Gly Ser Lys Val	Pro Phe Cys Pro Met
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Val Gly Ser Glu Val Tyr Ser	Ser Ser Glu Val Lys Lys	Thr Glu Val Leu
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Glu Val Tyr Glu Gly Glu Val	Thr Glu Leu Ser Pro Glu	Glu Ala Glu
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Ser Thr Thr Gly Gly Tyr Ala	Lys Ser Ile Ser His Val	Ile Ile Ser
145	150	155
Leu Lys Thr Val Lys Gly Thr	Lys Gln Leu Lys Leu Asp	Ser Ser Ile
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Tyr Asp Ala Leu Ile Lys Glu	Lys Val Ala Val Gly Asp	Val Ile Tyr
	180	185
Ile Glu Ala Asn Ser Gly Ala	Val Lys Arg Val Gly Arg	Cys Asp Ser
	195	200
Phe Ala Thr Glu Tyr Asp Leu	Glu Ala Glu Glu Tyr Val	Pro Ile Pro
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Lys Gly Glu Val His Lys Lys	Lys Glu Ile Val Gln Asp	Val Thr Leu
225	230	235
His Asp Leu Asp Ala Ala Asn	Ala Gln Pro Gln Gly Gly	Gln Asp Ile
	245	250
Leu Ser Leu Met Gly Gln Met	Met Lys Pro Arg Lys Thr	Glu Ile Thr
	260	265
Glu Lys Leu Arg Gln Glu Ile	Asn Lys Val Val Asn Arg	Tyr Ile Asp
	275	280
Glu Gly Ile Ala Glu Leu Val	Pro Gly Val Leu Phe Ile	Asp Glu Val
	290	295
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Ser Pro Leu Ser Pro Ile Val	Ile Leu Ala Thr Asn Arg	Gly Ile Cys
	325	330
Asn Val Arg Gly Thr Asp Met	Thr Ser Pro His Gly Ile	Pro Val Asp
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Glu Met Ile Gln Ile Leu Ala	Ile Arg Ala Gln Val Glu	Glu Ile Asp
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Met Asp Glu Glu Ser Leu Ala	Tyr Leu Gly Glu Ile Gly	Gln Gln Thr
385	390	395
Ser Leu Arg His Ala Ile Gln	Leu Ile Ser Pro Ala Ser	Val Val Ser
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Lys Thr Asn Gly Arg Glu Lys	Ile Cys Lys Ala Asp Leu	Glu Glu Val
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 <222> (82)...(1446)

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1 5 10	
aag aag cag cgc atc gcc acc cac act cac atc aag ggc ctc ggc ctc	159
Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly Leu	
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gac gcc aat gga atg tcg atg ccg ttg gcg gcg ggg ttc gtg ggc cag	207
Asp Ala Asn Gly Met Ser Met Pro Leu Ala Ala Gly Phe Val Gly Gln	
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gcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg atc cgc cag	255
Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg Gln	
45 50 55	
aag aag atg gcc ggt cgc gcg ctg ctc ctt gcg ggc ccg ccc gcc acg	303
Lys Lys Met Ala Gly Arg Ala Leu Leu Leu Ala Gly Pro Pro Ala Thr	
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Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser Lys	
75 80 85 90	
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Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Ser Glu Val	
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Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala Ile Gly Leu	
110 115 120	
cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt att gaa ctt	495
Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val Ile Glu Leu	
125 130 135	
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Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile	
140 145 150	
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Ser His Val Ile Ile Gly Leu Lys Thr Val Lys Gly Thr Lys Gln Leu	
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Lys Leu Asp Pro Ser Ile Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala	
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Val Gly Asp Val Ile Tyr Ile Glu Ala Asn Ser Gly Ala Val Lys Arg	
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Val Gly Arg Cys Asp Ser Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu	
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220 225 230	

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Val Asn Arg Tyr Ile Asp Glu Gly Ile Ala Glu Leu Val Pro Gly Val	
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Leu Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Tyr	
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His Gly Ile Pro Val Asp Leu Leu Asp Arg Leu Val Ile Ile Arg Thr	
350 355 360	
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Gln Val Glu Glu Ile Asp Ile Asp Glu Glu Ser Leu Ala Tyr Leu Gly	
380 385 390	
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Glu Ile Gly Gln Gln Thr Ser Leu Arg His Ala Ile Gln Leu Leu Ser	
395 400 405 410	
cct gcc agc gtg gtc gca aag acc aac ggg aga gaa aag atg tgc aag	1359
Pro Ala Ser Val Val Ala Lys Thr Asn Gly Arg Glu Lys Met Cys Lys	
415 420 425	
gct gac ctc gag gaa gtc agc ggg ctc tat ttg gat gcc aaa tcc tcg	1407
Ala Asp Leu Glu Glu Val Ser Gly Leu Tyr Leu Asp Ala Lys Ser Ser	
430 435 440	
gct cgc ctg ctc cag gag caa caa gaa aga tac atc acc tagacttgca	1456
Ala Arg Leu Leu Gln Glu Gln Glu Arg Tyr Ile Thr	
445 450 455	
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1876
 1886

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 Ala Leu Leu Leu Ala Gly Pro Pro Ala Thr Gly Lys Thr Ala Leu Ala
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 Val Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu
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 Met Glu Asn Phe Arg Arg Ala Ile Gly Leu Arg Ile Lys Glu Asn Lys
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 Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile Gly
 145 150 155 160
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 Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr
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 Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser
 195 200 205
 Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro
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 Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu
 225 230 235 240
 His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile
 245 250 255
 Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr
 260 265 270
 Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp
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 Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val
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 His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu
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 Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp
 370 375 380
 Ile Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr
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Ile Lys Gly Leu Gly Leu Asp Gln Ala Asn Gly Met Ser Met Pro Leu
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40 45 50

gcg gtc gac atg atc cgc cag aag aag atg gcc ggt cgc gcg ctg ctc 369
Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg Ala Leu Leu
55 60 65

ctt gcg ggc ccg ccc gcc acg ggc aaa acg gcg cta gcg ctc ggc ata 417
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Phe Arg Arg Ala Ile Gly Leu Arg Ile Lys Glu Asn Lys Glu Val Tyr
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Glu Gly Glu Val Ile Glu Leu Ser Pro Glu Glu Ala Glu Ser Thr Thr
135 140 145

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gtc Val 230	cat His	aag Lys	aaa Lys	aag Lys	gaa Glu	ata Ile 235	gtg Val	cag Gln	gat Asp	gtc Val	aca Thr 240	ctc Leu	cat His	gac Asp	ctt Leu	897
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Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu Gln Glu				
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Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro				
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Tyr Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp				
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Ser Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile				
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225 230 235 240				
Leu His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp				
245 250 255				
Ile Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile				
260 265 270				
Thr Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile				

275 280 285
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 Asp Leu Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro
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 Thr Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile
 370 375 380
 Asp Ile Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln
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 Ala Lys Thr Asn Gly Arg Glu Lys Met Cys Lys Ala Asp Leu Glu Glu
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 Met Arg Ile Glu Glu Val Gln Ser Thr Ser Lys Lys Gln Arg Ile
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 Ala Thr His Thr His Ile Lys Gly Leu Gly Leu Asp Ala Asn Gly Met
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 gcg att gcg ttg gcg gcg ggg ttc gtg ggc cag aag aag atg gcc ggc 204
 Ala Ile Ala Leu Ala Ala Gly Phe Val Gly Gln Lys Lys Met Ala Gly
 35 40 45

 cgc gcg gtg ctc ctt gcg ggt ccg ccc gcc acg ggc aag acg gcg cta 252
 Arg Ala Val Leu Leu Ala Gly Pro Pro Ala Thr Gly Lys Thr Ala Leu
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 gcg ggc ata gcc cag gag ctc ggc agc aag gtc cct ttc tgt cct atg 300
 Ala Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met
 65 70 75

 gta gga tca gaa gtg tac tcc tcg gag gtc aag aaa act gag gtg ctg 348
 Val Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu
 80 85 90 95

 atg gaa aat ttc cgt aga gct ata ggt ttg cgt ata aag gaa aac aaa 396
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 130 135 140

tta aag act gtt aaa ggg act aag caa ctg aag tta gat tct tca att 540
 Leu Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Ser Ser Ile
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tat gat gct ctg atc aag gaa aag gtg gca gtg ggt gat gtt ata tac 588
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 160 165 170 175

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 180 185 190

ttt gct aca gaa tac gat ctt gaa gct gaa gag tat gtt cct atc ccc 684
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 210 215 220

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 225 230 235

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 Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr
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gaa aaa cta cgc caa gaa att aat aag gtg gta aat aga tat atc gat 876
 Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp
 260 265 270

gaa gga att gca gag ctt gta cct ggt gtt ttg ttc att gat gag gtc 924
 Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val
 275 280 285

cac atg ttg gat atc gaa tgt ttt tct tat ctt aac cgt gca ttg gag 972
 His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu
 290 295 300

agc cca tta tca cca atc gtg ata ctt gct aca aat agg gga ata tgt 1020
 Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys
 305 310 315

aat gta aga gga act gat atg aca agt cca cat ggt ata ccg gtg gat 1068
 Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val Asp
 320 325 330 335

ctt cta gat agg ctg gtg att att cgg aca gag aca tat ggc cct act 1116
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 370 375 380

tct ttg aga cat gct att caa ttg ata tca cct gcc agc gtg gtc tca 1260
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 385 390 395

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 Lys Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val
 400 405 410 415

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caa caa gaa aga tac atc acc tagatttggg tcacctgtcg tggaagtctc 1407
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 35 40 45
 Ala Val Leu Leu Ala Gly Pro Pro Ala Thr Gly Lys Thr Ala Leu Ala
 50 55 60
 Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met Val
 65 70 75 80
 Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu Met
 85 90 95
 Glu Asn Phe Arg Arg Ala Ile Gly Leu Arg Ile Lys Glu Asn Lys Glu
 100 105 110
 Val Tyr Glu Gly Glu Val Thr Glu Leu Ser Pro Glu Glu Ala Glu Ser
 115 120 125
 Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile Ser Leu
 130 135 140
 Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Ser Ser Ile Tyr
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 Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr Ile
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 Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser Phe

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 225 230 235 240
 Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr Glu
 245 250 255
 Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp Glu
 260 265 270
 Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val His
 275 280 285
 Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu Ser
 290 295 300
 Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys Asn
 305 310 315 320
 Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val Asp Leu
 325 330 335
 Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro Thr Glu
 340 345 350
 Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp Met
 355 360 365
 Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr Ser
 370 375 380
 Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser Lys
 385 390 395 400
 Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val Ser
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 Gly Leu Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu Gln
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 Gln Glu Arg Tyr Ile Thr
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 <213> Artificial Sequence

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 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

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